SEQUENCE LISTING

<110> Cases, Sylvaine
Stone, Scot
Zhou, Ping
Farese, Robert V.
Chi-Liang Eric Yen

<120> MONO- AND DIACYGLYCEROL ACYLTRANSFERASES AND METHODS OF USE THEREOF

<130> UCAL240CIP

<140> Unassigned
<141> 2002-01-14

<150> 60/271,307
<151> 2001-02-23

<150> 09/794,715
<151> 2001-02-26

<160> 18

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1231
<212> DNA
<213> Homo sapiens

<400> 1
ttcagccatg aagaccctca tagccgccta ctccggggtc ctgcgcggcg agcgtcaggc 60
cgaggctgac cggagccagc gctctcacgg aggacccgtg tcgcgcgagg ggtctgggag 120
atggggcact ggatccagca tcctctccgc cctccaggac ctcttctctg tcacctggct 180
caataggtcc aaggtggaaa agcagctaca ggtcatctca gtgctccagt gggtcctgtc 240
cttccttgta ctgggagtgg cctgcagtgc catcctcatg tacatattct gcactgattg 300
ctggctcatc gctgtgctct acttcacttg gctggtgttt gactggaaca cacccaagaa 360
aggtggcagg aggtcacagt gggtccgaaa ctgggctgtg tggcgctact ttcgagacta 420
ctttcccatc cagctggtga agacacacaa cctgctgacc accaggaact atatctttgg 480
ataccacccc catggtatca tgggcctggg tgccttctgc aacttcagca cagaggccac 540
agaagtgagc aagaagttcc caggcatacg gccttacctg gctacactgg caggcaactt 600
ccgaatgcct gtgttgaggg agtacctgat gtctggaggt atctgccctg tcagccggga 660
caccatagac tatttgcttt caaagaatgg gagtggcaat gctatcatca tcgtggtcgg 720
gggtgcggct gagtctctga gctccatgcc tggcaagaat gcagtcaccc tgcggaaccg 780
caagggcttt gtgaaactgg ccctgcgtca tggagctgac ctggttccca tctactcctt 840
tggagagaat gaagtgtaca agcaggtgat cttcgaggag ggctcctggg gccgatgggt 900
ccagaagaag ttccagaaat acattggttt cgccccatgc atcttccatg gtcgaggcct 960
cttctcctcc gacacctggg ggctggtgcc ctactccaag cccatcacca ctgttgtggg 1020
agagcccatc accatcccca agctggagca cccaacccag caagacatcg acctgtacca 1080
caccatgtac atggaggccc tggtgaagct cttcgacaag cacaagacca agttcggcct 1140

caccatgtac atggaggccc tggtgaagct cttcgacaag cacaagacca agttcggcct 1140
cccggagact gaggtcctgg aggtgaactg agccagcctt cggggccaat tccctggagg 1200
aaccagctgc aaatcacttt tttgctctgt a 1231

<210> 2
<211> 388
<212> PRT
<213> Homo sapiens

<400> 2

```
Met Lys Thr Leu Ile Ala Ala Tyr Ser Gly Val Leu Arg Gly Glu Arg
 1               5                  10                  15
Gln Ala Glu Ala Asp Arg Ser Gln Arg Ser His Gly Gly Pro Ala Leu
            20                  25                  30
Ser Arg Glu Gly Ser Gly Arg Trp Gly Thr Gly Ser Ser Ile Leu Ser
        35                  40                  45
Ala Leu Gln Asp Leu Phe Ser Val Thr Trp Leu Asn Arg Ser Lys Val
    50                  55                  60
Glu Lys Gln Leu Gln Val Ile Ser Val Leu Gln Trp Val Leu Ser Phe
65                  70                  75                  80
Leu Val Leu Gly Val Ala Cys Ser Ala Ile Leu Met Tyr Ile Phe Cys
                85                  90                  95
Thr Asp Cys Trp Leu Ile Ala Val Leu Tyr Phe Thr Trp Leu Val Phe
            100                 105                 110
Asp Trp Asn Thr Pro Lys Lys Gly Gly Arg Arg Ser Gln Trp Val Arg
        115                 120                 125
Asn Trp Ala Val Trp Arg Tyr Phe Arg Asp Tyr Phe Pro Ile Gln Leu
    130                 135                 140
Val Lys Thr His Asn Leu Leu Thr Thr Arg Asn Tyr Ile Phe Gly Tyr
145                 150                 155                 160
His Pro His Gly Ile Met Gly Leu Gly Ala Phe Cys Asn Phe Ser Thr
                165                 170                 175
Glu Ala Thr Glu Val Ser Lys Lys Phe Pro Gly Ile Arg Pro Tyr Leu
            180                 185                 190
Ala Thr Leu Ala Gly Asn Phe Arg Met Pro Val Leu Arg Glu Tyr Leu
        195                 200                 205
Met Ser Gly Gly Ile Cys Pro Val Ser Arg Asp Thr Ile Asp Tyr Leu
    210                 215                 220
Leu Ser Lys Asn Gly Ser Gly Asn Ala Ile Ile Ile Val Val Gly Gly
225                 230                 235                 240
Ala Ala Glu Ser Leu Ser Ser Met Pro Gly Lys Asn Ala Val Thr Leu
                245                 250                 255
Arg Asn Arg Lys Gly Phe Val Lys Leu Ala Leu Arg His Gly Ala Asp
            260                 265                 270
Leu Val Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr Lys Gln Val
        275                 280                 285
Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln Lys Lys Phe Gln
    290                 295                 300
Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His Gly Arg Gly Leu Phe
305                 310                 315                 320
Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr Ser Lys Pro Ile Thr Thr
```

```
                325                 330                 335
Val Val Gly Glu Pro Ile Thr Ile Pro Lys Leu Glu His Pro Thr Gln
            340                 345                 350
Gln Asp Ile Asp Leu Tyr His Thr Met Tyr Met Glu Ala Leu Val Lys
        355                 360                 365
Leu Phe Asp Lys His Lys Thr Lys Phe Gly Leu Pro Glu Thr Glu Val
    370                 375                 380
Leu Glu Val Asn
385
```

<210> 3
<211> 1167
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)...(1167)
<223> n = A,T,C or G

<400> 3

```
atgaagaccc tcatcgccgc ctactccggg gtcctgcggg gtgagcgtcg ggcggaagct      60
gcccgcagcg aaaacaagaa taaaggatct gccctgtcac gcgaggggtc tgggcgatgg     120
ggcactggct ccagcatcct ctcagccctc caagacatct tctctgtcac ctggctcaac     180
agatcyaagg tggaaaaaca gctgcaggtc atctcagtac tacaatgggt cctatccttc     240
ctggtgctag gagtggcctg cagtgtcatc ctcatgtaca ccttctgcac agactgctgg     300
ctgatagctg tgctctactt cacctggctg gcatttgact ggaacacgcc caagaaaggt     360
ggcaggagat cgcagtgggt gcgaaactgg gccgtgtggc gctacttccg agactacttt     420
cccatccagc tggtgaagac acacaacctg ctgaccacca ggaactatat ctttggatac     480
caccccatg gcatcatggg cctgggtgcc ttctgtaact tcagcacaga ggctactgaa      540
gtcagcaaga agtttcctgg cataaggccc tatttggcta cgttggcygg taacttccgg     600
atgcctgtgc ttcgcgagta cctgatgtct ggaggcatct gccctgtcaa ccgagacacc     660
atagactact tgctctccaa gaatgggagt ggcaatgcta tcatcatcgt ggtgggaggt     720
gcagctgagt ccctgagctc catgcctggc aagaacgcag tcaccctgaa gaaccgcaaa     780
ggctttgtga agctggccct gcgccatgga gctgatctgg ttcccactta ttcctttgga     840
gagaatgagg tatacaagca ggtgatcttt gaggagggtt cctggggccg atgggtccag     900
aagaagttcc agaagtatat tggtttcgcc ccctgcatct tccatggccg aggcctcttc     960
tcctctgaca cctgggggct ggtgccctac tccaagccca tcaccaccgt cgtgggggag    1020
cccatcactg tccccaagct ggagcacccg acccagaaag acatcgacct gtaccatgcc    1080
atgtacatgg aggccctggt gaagctcttt gacaatcaca agaccaaatt tggcctncca    1140
gagactgagg tgctggaggt gaactga                                        1167
```

<210> 4
<211> 387
<212> PRT
<213> Mus musculus

<400> 4

```
Met Lys Thr Leu Ile Ala Ala Tyr Ser Gly Val Leu Arg Gly Glu Arg
 1               5                  10                  15
Arg Ala Glu Leu Pro Ala Ala Lys Asn Lys Asn Lys Gly Ser Ala Leu
```

```
            20                  25                  30
Ser Arg Glu Gly Ser Gly Arg Trp Gly Thr Gly Ser Ser Ile Leu Ser
        35                  40                  45
Ala Leu Gln Asp Ile Phe Ser Val Thr Trp Leu Asn Arg Ser Lys Val
    50                  55                  60
Glu Lys Gln Leu Gln Val Ile Ser Val Leu Gln Trp Val Leu Ser Phe
65                  70                  75                  80
Leu Val Leu Gly Val Ala Cys Ser Val Ile Leu Met Tyr Thr Phe Cys
                85                  90                  95
Thr Asp Cys Trp Leu Ile Ala Val Leu Tyr Phe Thr Trp Leu Ala Phe
            100                 105                 110
Asp Trp Asn Thr Pro Lys Lys Gly Gly Arg Arg Ser Gln Trp Val Arg
        115                 120                 125
Asn Trp Ala Val Trp Arg Tyr Phe Arg Asp Tyr Phe Pro Ile Gln Leu
    130                 135                 140
Val Lys Thr His Asn Leu Leu Thr Thr Arg Asn Tyr Ile Phe Gly Tyr
145                 150                 155                 160
His Pro His Gly Ile Met Gly Leu Gly Ala Phe Cys Asn Phe Ser Thr
                165                 170                 175
Glu Ala Thr Glu Val Ser Lys Lys Phe Pro Gly Ile Arg Pro Tyr Leu
            180                 185                 190
Ala Thr Leu Ala Gly Asn Phe Arg Met Pro Val Leu Arg Glu Tyr Leu
        195                 200                 205
Met Ser Gly Gly Ile Cys Leu Val Asn Arg Asp Thr Ile Asp Tyr Leu
    210                 215                 220
Leu Ser Lys Asn Gly Ser Gly Asn Ala Ile Ile Ile Val Val Gly Gly
225                 230                 235                 240
Ala Ala Glu Ser Leu Ser Ser Met Pro Gly Lys Asn Ala Val Thr Leu
                245                 250                 255
Lys Asn Arg Lys Gly Phe Val Lys Leu Ala Leu Arg His Gly Ala Asp
            260                 265                 270
Leu Val Pro Thr Tyr Ser Phe Gly Glu Asn Glu Val Tyr Lys Gln Val
        275                 280                 285
Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Lys Lys Phe Gln Lys
    290                 295                 300
Tyr Ile Gly Phe Ala Pro Cys Ile Phe His Gly Arg Gly Leu Phe Ser
305                 310                 315                 320
Ser Asp Thr Trp Gly Leu Val Pro Tyr Ser Lys Pro Ile Thr Thr Val
                325                 330                 335
Val Gly Glu Pro Ile Thr Val Pro Lys Leu Glu His Pro Thr Gln Lys
            340                 345                 350
Asp Ile Asp Leu Tyr His Ala Met Tyr Met Glu Ala Leu Val Lys Leu
        355                 360                 365
Phe Asp Asn His Lys Thr Lys Phe Gly Leu Pro Glu Thr Glu Val Leu
    370                 375                 380
Glu Val Asn
385
```

<210> 5
<211> 1008
<212> DNA

<213> Mus musculus

<400> 5
atgatggtcg agttcgcgcc actcaacacc ccgctggcac ggtgcctaca gaccgctgcg 60
gtgctgcagt gggtcctgtc cttcctcctg ctcgtgcagg tgtgcattgg aattatggtg 120
atgctggtcc tgtacaacta ttggttcctt tacatcccat atctggtctg gttttactat 180
gactggagaa ccccagagca aggaggcaga agatggaact gggtccaaag ctggcctgtg 240
tggaagtatt ttaaggagta ttttccaatc tgtcttgtca aaacgcagga tttggatccg 300
ggtcacaatt atatatttgg gtttcaccct catggaatat tcgtgcctgg agcctttgga 360
aatttttgta caaaatactc ggacttcaag aagctatttc ctggctttac atcgtatctc 420
cacgtggcca agatctggtt ctgtttcccg ttgttccgag aatatctgat gagtaacggg 480
ccggtttcag tgtctaagga gagtttgtct catgtgctga gcaaggatgg aggtggcaat 540
gtctcaatca ttgtcctcgg aggtgcaaag gaggcgctgg aggctcaccc aggaacattc 600
accctgtgca tccgccagcg caaagggttt gttaagatgg ccttgaccca tggtgccagt 660
ttggttccag tattttcttt tggtgaaaat gatctatata agcaaattaa caaccccaaa 720
ggctcctggc tacgaactat acaagacgca atgtatgatt caatgggagt agccttgcca 780
ctgatatatg ccagaggaat tttccagcac tactttggca taatgcccta tcggaagctg 840
atctacactg ttgttggccg ccctatccct gttcagcaga ttctgaaccc gacctcagag 900
cagattgaag agctgcatca gacataccta gaggagctaa agaaactatt caatgaacac 960
aaagggaaat atgggattcc ggagcacgaa actctggtat ttaaataa 1008

<210> 6
<211> 335
<212> PRT
<213> Mus musculus

<400> 6
Met Met Val Glu Phe Ala Pro Leu Asn Thr Pro Leu Ala Arg Cys Leu
1 5 10 15
Gln Thr Ala Ala Val Leu Gln Trp Val Leu Ser Phe Leu Leu Leu Val
20 25 30
Gln Val Cys Ile Gly Ile Met Val Met Leu Val Leu Tyr Asn Tyr Trp
35 40 45
Phe Leu Tyr Ile Pro Tyr Leu Val Trp Phe Tyr Tyr Asp Trp Arg Thr
50 55 60
Pro Glu Gln Gly Gly Arg Arg Trp Asn Trp Val Gln Ser Trp Pro Val
65 70 75 80
Trp Lys Tyr Phe Lys Glu Tyr Phe Pro Ile Cys Leu Val Lys Thr Gln
85 90 95
Asp Leu Asp Pro Gly His Asn Tyr Ile Phe Gly Phe His Pro His Gly
100 105 110
Ile Phe Val Pro Gly Ala Phe Gly Asn Phe Cys Thr Lys Tyr Ser Asp
115 120 125
Phe Lys Lys Leu Phe Pro Gly Phe Thr Ser Tyr Leu His Val Ala Lys
130 135 140
Ile Trp Phe Cys Phe Pro Leu Phe Arg Glu Tyr Leu Met Ser Asn Gly
145 150 155 160
Pro Val Ser Val Ser Lys Glu Ser Leu Ser His Val Leu Ser Lys Asp
165 170 175
Gly Gly Gly Asn Val Ser Ile Ile Val Leu Gly Gly Ala Lys Glu Ala
180 185 190

```
Leu Glu Ala His Pro Gly Thr Phe Thr Leu Cys Ile Arg Gln Arg Lys
        195                 200                 205
Gly Phe Val Lys Met Ala Leu Thr His Gly Ala Ser Leu Val Pro Val
    210                 215                 220
Phe Ser Phe Gly Glu Asn Asp Leu Tyr Lys Gln Ile Asn Asn Pro Lys
225                 230                 235                 240
Gly Ser Trp Leu Arg Thr Ile Gln Asp Ala Met Tyr Asp Ser Met Gly
                245                 250                 255
Val Ala Leu Pro Leu Ile Tyr Ala Arg Gly Ile Phe Gln His Tyr Phe
            260                 265                 270
Gly Ile Met Pro Tyr Arg Lys Leu Ile Tyr Thr Val Val Gly Arg Pro
        275                 280                 285
Ile Pro Val Gln Gln Ile Leu Asn Pro Thr Ser Glu Gln Ile Glu Glu
    290                 295                 300
Leu His Gln Thr Tyr Leu Glu Glu Leu Lys Lys Leu Phe Asn Glu His
305                 310                 315                 320
Lys Gly Lys Tyr Gly Ile Pro Glu His Glu Thr Leu Val Phe Lys
                325                 330                 335
```


<210> 7
<211> 1129
<212> DNA
<213> Homo sapiens

<400> 7

```
cgtgggtgca ggctgcagtg gctggcgccg tcctcgcccg gccaggccat gaaggtagag      60
tttgcaccgc tcaacatcca gctggcgcgg cggctgcaga cggtggccgt gctgcagtgg     120
gtccttttctt ttcttacagg gccgatgtcc attggaatca ctgtgatgct gatcatacac     180
aactatttgt tcctttacat cccttatttg atgtggcttt actttgactg gcatacccca     240
gagcgaggag gcaggagatc cagctggatc aaaaattgga ctctttggaa acactttaag     300
gactattttc caattcatct tatcaaaact caagatttgg atccaagtca caactatata     360
tttgggtttc acccccatgg aataatggca gttggagcct ttgggaattt ttctgtaaat     420
tattctgact tcaaggacct gtttcctggc tttacttcat atcttcacgt gctgccactt     480
tggttctggt gtcctgtctt tcgagaatat gtgatgagtg ttgggctggt ttcagtttcc     540
aagaaaagtg tgtcctacat ggtaagcaag gagggaggtg gaaacatctc tgtcattgtc     600
cttgggggtg caaaagaatc actggatgct catcctggaa agttcactct gttcatccgc     660
cagcggaaag gatttgttaa aattgctttg acccatggcg cctctctggt cccagtggtt     720
tcttttggtg aaaatgaact gtttaaacaa actgacaacc ctgaaggatc atggattaga     780
actgttcaga ataaactgca gaagatcatg gggtttgctt tgcccctgtt tcatgccagg     840
ggagtttttc agtacaattt tggcctaatg acctatagga aagccatcca cactgttgtt     900
ggccgcccga tccctgttcg tcagactctg aacccgaccc aggagcagat tgaggagtta     960
catcagacct atatggagga acttaggaaa ttgtttgagg aacacaaagg aaagtatggc    1020
attccagagc acgagactct tgttttaaaa tgacttgact ataaaaaaaa attaaaaaat    1080
aaaaataaat gacttggctg taataaggca taaagaagga taagagacc                1129
```

<210> 8
<211> 334
<212> PRT
<213> Homo sapiens

<400> 8

```
Met Lys Val Glu Phe Ala Pro Leu Asn Ile Gln Leu Ala Arg Arg Leu
 1               5                  10                  15
Gln Thr Val Ala Val Leu Gln Trp Val Leu Ser Phe Leu Thr Gly Pro
            20                  25                  30
Met Ser Ile Gly Ile Thr Val Met Leu Ile Ile His Asn Tyr Leu Phe
        35                  40                  45
Leu Tyr Ile Pro Tyr Leu Met Trp Leu Tyr Phe Asp Trp His Thr Pro
    50                  55                  60
Glu Arg Gly Gly Arg Arg Ser Ser Trp Ile Lys Asn Trp Thr Leu Trp
65                  70                  75                  80
Lys His Phe Lys Asp Tyr Phe Pro Ile His Leu Ile Lys Thr Gln Asp
                85                  90                  95
Leu Asp Pro Ser His Asn Tyr Ile Phe Gly Phe His Pro His Gly Ile
            100                 105                 110
Met Ala Val Gly Ala Phe Gly Asn Phe Ser Val Asn Tyr Ser Asp Phe
        115                 120                 125
Lys Asp Leu Phe Pro Gly Phe Thr Ser Tyr Leu His Val Leu Pro Leu
    130                 135                 140
Trp Phe Trp Cys Pro Val Phe Arg Glu Tyr Val Met Ser Val Gly Leu
145                 150                 155                 160
Val Ser Val Ser Lys Lys Ser Val Ser Tyr Met Val Ser Lys Glu Gly
                165                 170                 175
Gly Gly Asn Ile Ser Val Ile Val Leu Gly Gly Ala Lys Glu Ser Leu
            180                 185                 190
Asp Ala His Pro Gly Lys Phe Thr Leu Phe Ile Arg Gln Arg Lys Gly
        195                 200                 205
Phe Val Lys Ile Ala Leu Thr His Gly Ala Ser Leu Val Pro Val Val
    210                 215                 220
Ser Phe Gly Glu Asn Glu Leu Phe Lys Gln Thr Asp Asn Pro Glu Gly
225                 230                 235                 240
Ser Trp Ile Arg Thr Val Gln Asn Lys Leu Gln Lys Ile Met Gly Phe
                245                 250                 255
Ala Leu Pro Leu Phe His Ala Arg Gly Val Phe Gln Tyr Asn Phe Gly
            260                 265                 270
Leu Met Thr Tyr Arg Lys Ala Ile His Thr Val Val Gly Arg Pro Ile
        275                 280                 285
Pro Val Arg Gln Thr Leu Asn Pro Thr Gln Glu Gln Ile Glu Glu Leu
    290                 295                 300
His Gln Thr Tyr Met Glu Glu Leu Arg Lys Leu Phe Glu Glu His Lys
305                 310                 315                 320
Gly Lys Tyr Gly Ile Pro Glu His Glu Thr Leu Val Leu Lys
                325                 330
```

<210> 9
<211> 435
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)...(435)

<223> n = A,T,C or G

<400> 9
ttacctccct cagggtcctg ggcatcatgt cttgctctat gaagactgaa cacttacaga 60
gtctgagcct tctgcagtgg cccttgagct acgttgccat gttttggatt gtgcagccat 120
tgttaatttg cctattgttc acacccttgt ggccgctacc aacagtttac tttgtctggt 180
tacttctcga ctggaagact ccagataaag gtggcaggcg ttcagactgg gtacggaact 240
ggaatgtctg gaaccacatc agggactatt tccccattac aatcctgaag actaaggacc 300
tgtcaccttc agagaactac atcatggggg tccaccccat nggtctcctg accttcggtg 360
ccttctgcaa cttctgcact gaggccacag gcttctcgaa gaccttccca ggcatcactc 420
ctcacttggc cacac 435

<210> 10
<211> 229
<212> PRT
<213> Mus musculus

<400> 10
Met Lys Thr Glu His Leu Gln Ser Leu Ser Leu Leu Gln Trp Pro Leu
1 5 10 15
Ser Tyr Val Ala Met Phe Trp Ile Val Gln Pro Leu Leu Ile Cys Leu
20 25 30
Leu Phe Thr Pro Leu Trp Pro Leu Pro Thr Val Tyr Phe Val Trp Leu
35 40 45
Leu Leu Asp Trp Lys Thr Pro Asp Lys Gly Gly Arg Arg Ser Asp Trp
50 55 60
Val Arg Asn Trp Asn Val Trp Asn His Ile Arg Asp Tyr Phe Pro Ile
65 70 75 80
Thr Ile Leu Lys Thr Lys Asp Leu Ser Pro Ser Glu Asn Tyr Ile Met
85 90 95
Gly Val His Pro His Gly Leu Leu Thr Phe Gly Ala Phe Cys Asn Phe
100 105 110
Cys Thr Glu Ala Thr Gly Phe Ser Lys Thr Phe Pro Gly Ile Thr Pro
115 120 125
His Leu Ala Thr Leu Ser Trp Phe Phe Lys Ile Pro Ile Ile Arg Asp
130 135 140
Tyr Ile Met Ala Lys Gly Leu Cys Ser Val Ser Gln Ala Ser Ile Asp
145 150 155 160
Tyr Leu Leu Ser His Gly Thr Gly Asn Leu Val Gly Ile Pro Ile Ile
165 170 175
Thr Val Val Gly Glu Ala Leu Pro Leu Pro Gln Val Lys Asn Pro Ser
180 185 190
Pro Glu Ile Val Asp Lys Tyr His Ala Leu Tyr Met Asp Ala Leu Tyr
195 200 205
Lys Leu Phe Glu Gln His Lys Val Gln Tyr Gly Cys Ser Asn Thr Gln
210 215 220
Lys Leu Ile Phe Leu
225

<210> 11
<211> 1240

<212> DNA
<213> Homo sapiens

<400> 11
atcaactcag cttaagaagt tttggccttc tggttaggct tcttgccaca acagaacagc 60
accataacca tggctttctt ctcccgactg aatctccagg agggcctcca aaccttcttt 120
gttttgcaat ggatcccagt ctatatattt ttagtttgga tcttgcagcc attgttcgtc 180
tacctgctgt ttacatcctt gtggccgcta ccagtgcttt actttgcctg gttgttcctg 240
gactggaaga ccccagagcg aggtggcagg cgttcggcct gggtaaggaa ctggtgtgtc 300
tggacccaca tcagggacta tttccccatt acgatcctga agacaaagga cctatcacct 360
gagcacaact acctcatggg ggttcacccc catggcctcc tgacctttgg cgccttctgc 420
aacttctgca ctgaggccac aggcttctcg aagaccttcc caggcatcac tcctcacttg 480
gccacgctgt cctggttctt caagatcccc tttgttaggg agtacctcat ggccaaaggt 540
gtgtgctctg tgagccagcc agccatcaac tatctgctga gccatggcac tggcaacctc 600
gtgggcattg tagtgggagg tgtgggtgag gccctgcaaa gtgtgcccaa caccaccacc 660
ctcatcctcc agaagcgcaa ggggttcgtg cgcacagccc tccagcatgg ggcatacctt 720
gtcccttcat attcctttgg tgagaacgaa gttttcaatc aggagacctt ccctgagggc 780
acgtggttaa ggttgttcca aaaaaccttc caggacacat tcaaaaaaat cctgggacta 840
aatttctgta ccttccatgg ccggggcttc actcgcggat cctggggctt cctgcctttc 900
aatcggccca ttaccactgt tgttggggaa ccccttccaa ttcccaggat taagaggcca 960
aaccagaaga cagtagacaa gtatcacgca ctctacatca gtgccctgcg caagctcttt 1020
gaccaacaca aagttgaata tggcctccct gagacccaag agctgacaat tacataacag 1080
gagccacatt ccccattgat caaccccccaa agccatgagg gatccaagta gagccacaga 1140
aaaagaagaa ttccaggaga gggaaagatc gtaaggatga gagaggagac catccaagcc 1200
agaaattatt taataaatca gagttctagc aatagagtcc 1240

<210> 12
<211> 335
<212> PRT
<213> Homo sapiens

<400> 12
Met Ala Phe Phe Ser Arg Leu Asn Leu Gln Glu Gly Leu Gln Thr Phe
1 5 10 15
Phe Val Leu Gln Trp Ile Pro Val Tyr Ile Phe Leu Val Trp Ile Leu
20 25 30
Gln Pro Leu Phe Val Tyr Leu Leu Phe Thr Ser Leu Trp Pro Leu Pro
35 40 45
Val Leu Tyr Phe Ala Trp Leu Phe Leu Asp Trp Lys Thr Pro Glu Arg
50 55 60
Gly Gly Arg Arg Ser Ala Trp Val Arg Asn Trp Cys Val Trp Thr His
65 70 75 80
Ile Arg Asp Tyr Phe Pro Ile Thr Ile Leu Lys Thr Lys Asp Leu Ser
85 90 95
Pro Glu His Asn Tyr Leu Met Gly Val His Pro His Gly Leu Leu Thr
100 105 110
Phe Gly Ala Phe Cys Asn Phe Cys Thr Glu Ala Thr Gly Phe Ser Lys
115 120 125
Thr Phe Pro Gly Ile Thr Pro His Leu Ala Thr Leu Ser Trp Phe Phe
130 135 140
Lys Ile Pro Phe Val Arg Glu Tyr Leu Met Ala Lys Gly Val Cys Ser

```
145                 150                 155                 160
Val Ser Gln Pro Ala Ile Asn Tyr Leu Leu Ser His Gly Thr Gly Asn
                165                 170                 175
Leu Val Gly Ile Val Val Gly Gly Val Gly Glu Ala Leu Gln Ser Val
            180                 185                 190
Pro Asn Thr Thr Thr Leu Ile Leu Gln Lys Arg Lys Gly Phe Val Arg
        195                 200                 205
Thr Ala Leu Gln His Gly Ala Tyr Leu Val Pro Ser Tyr Ser Phe Gly
    210                 215                 220
Glu Asn Glu Val Phe Asn Gln Glu Thr Phe Pro Glu Gly Thr Trp Leu
225                 230                 235                 240
Arg Leu Phe Gln Lys Thr Phe Gln Asp Thr Phe Lys Lys Ile Leu Gly
                245                 250                 255
Leu Asn Phe Cys Thr Phe His Gly Arg Gly Phe Thr Arg Gly Ser Trp
            260                 265                 270
Gly Phe Leu Pro Phe Asn Arg Pro Ile Thr Thr Val Val Gly Glu Pro
        275                 280                 285
Leu Pro Ile Pro Arg Ile Lys Arg Pro Asn Gln Lys Thr Val Asp Lys
    290                 295                 300
Tyr His Ala Leu Tyr Ile Ser Ala Leu Arg Lys Leu Phe Asp Gln His
305                 310                 315                 320
Lys Val Glu Tyr Gly Leu Pro Glu Thr Gln Glu Leu Thr Ile Thr
                325                 330                 335
```

<210> 13
<211> 1872
<212> DNA
<213> Homo sapiens

<400> 13

```
aattcggctt actcactata gggctcgagc ggcccccggg caggtgccga cttcatttcc      60
aagtctgcac acaatgcagg cagtagccat gcctgacagc cacatgacag atactacacc     120
gctgaatgtg ctctaaccct ggacttggca ttgcccctac tgttgaggaa gcagtgcgtt     180
tttctccagt ctttcaggtc ccttcaccag ggaaccatta acttgtgcat cagaacaagg     240
acatttcctt acattcctgc aaacacagtc ctttcagttt actctttttt tgaggggggg     300
gcgcggggaa cggagtctcg ctctgtcgcc caggctggag tgcaatggtg caatctcagc     360
tcactgcaac ctctgcctcc caggtccaag cgattctcct gcctcagcct cccgggtagc     420
cgggactaca ggcgcctgcc accacgcccg gctaattttt gtatttttag tagagacgag     480
gtttcgccgt gttggcaggc tggtcttgga actcctgacc tcaggtgatt tactcgcctc     540
ggcctcccaa agtgctggga ttacaggcat gagccactgt gcccagtcac aagtttttat     600
tttagccatt ttgataagtg tgaagttccc tgatggctaa tgatgttcct ttttccatgt     660
gctcatttgt catctatgcc agagaagatt tggagaggag gacgtgaatt ggaggaaaac     720
tgttccagga ttccccacct ctggtggccc accgctggct cactgccatt gaccacactg     780
caggcagagc ctagtgcagt gctggagcag ggcccagaga ggagagggct tacagtgtga     840
attcagctca gctggggaag aagacacctt cccttctaga cctgaatcgg gttcccaagc     900
aaccactgtg attgctgtca acctctacct ggtggtgttc acaccatact ggcctgtcac     960
tgtgcttatt cttacctggc tggcttttga ctggaagacc cctcagcgag gcggccgccg    1020
gtttacctgt gtgaggcact ggcgcctgtg gaaacactac agcgattatt tccctctcaa    1080
gcttctgaag actcatgaca tctgccccag ccgcaactac atcctcgtct gccaccctca    1140
tgggctcttt gcccatggat ggtttggcca ctttgccaca gaggcctcag gcttctccaa    1200
gatatttcct ggcatcaccc cttacatact cacactggga gccttttttct ggatgccttt    1260
```

cctcagagaa tatgtaatgt ctacaggggc ctgctctgtg agtcgatcct ccattgactt 1320
tctgctgact cataaaggca caggcaacat ggtcattgtg gtgattggtg gactggctga 1380
gtgcagatac agcctgccag gttcttctac cctggtgttg aagaaccggt ctggctttgt 1440
gcgcatggcc cttcagcatg gggtgcctct aatacctgcc tatgcctttg ggggagacgga 1500
cctctatgat cagcacattt tcactcctgg tggctttgtc aaccgcttcc agaagtggtt 1560
ccagagcatg gtacacatct accettgtgc tttctatgga cgtggcttca ccaagaactc 1620
ctggggcctt ctgccctata gtcggcctgt aaccaccatc gtcggggagc ctctaccaat 1680
gcccaagatt gagaatccaa gccaggagat cgtggctaaa tatcacacac tctatattga 1740
tgccctacgt aaactgtttg accagcataa gaccaagttt ggtatctcag agacccagga 1800
gctggagata atttgacaga catccccagt agccttcacc ctggctggaa ggtatggatg 1860
gacccagtga ga 1872

<210> 14
<211> 333
<212> PRT
<213> Homo sapiens

<400> 14
Met Leu Leu Pro Ser Lys Lys Asp Leu Lys Thr Ala Leu Asp Val Phe
1 5 10 15
Ala Val Phe Gln Trp Ser Phe Ser Ala Leu Leu Ile Thr Thr Thr Val
20 25 30
Ile Ala Val Asn Leu Tyr Leu Val Val Phe Thr Pro Tyr Trp Pro Val
35 40 45
Thr Val Leu Ile Leu Thr Trp Leu Ala Phe Asp Trp Lys Thr Pro Gln
50 55 60
Arg Gly Gly Arg Arg Phe Thr Cys Val Arg His Trp Arg Leu Trp Lys
65 70 75 80
His Tyr Ser Asp Tyr Phe Pro Leu Lys Leu Leu Lys Thr His Asp Ile
85 90 95
Cys Pro Ser Arg Asn Tyr Ile Leu Val Cys His Pro His Gly Leu Phe
100 105 110
Ala His Gly Trp Phe Gly His Phe Ala Thr Glu Ala Ser Gly Phe Ser
115 120 125
Lys Ile Phe Pro Gly Ile Thr Pro Tyr Ile Leu Thr Leu Gly Ala Phe
130 135 140
Phe Trp Met Pro Phe Leu Arg Glu Tyr Val Met Ser Thr Gly Ala Cys
145 150 155 160
Ser Val Ser Arg Ser Ser Ile Asp Phe Leu Leu Thr His Lys Gly Thr
165 170 175
Gly Asn Met Val Ile Val Val Ile Gly Gly Leu Ala Glu Cys Arg Tyr
180 185 190
Ser Leu Pro Gly Ser Ser Thr Leu Val Leu Lys Asn Arg Ser Gly Phe
195 200 205
Val Arg Met Ala Leu Gln His Gly Val Pro Leu Ile Pro Ala Tyr Ala
210 215 220
Phe Gly Glu Thr Asp Leu Tyr Asp Gln His Ile Phe Thr Pro Gly Gly
225 230 235 240
Phe Val Asn Arg Phe Gln Lys Trp Phe Gln Ser Met Val His Ile Tyr
245 250 255
Pro Cys Ala Phe Tyr Gly Arg Gly Phe Thr Lys Asn Ser Trp Gly Leu

```
            260                 265                 270
Leu Pro Tyr Ser Arg Pro Val Thr Thr Ile Val Gly Glu Pro Leu Pro
        275                 280                 285
Met Pro Lys Ile Glu Asn Pro Ser Gln Glu Ile Val Ala Lys Tyr His
    290                 295                 300
Thr Leu Tyr Ile Asp Ala Leu Arg Lys Leu Phe Asp Gln His Lys Thr
305                 310                 315                 320
Lys Phe Gly Ile Ser Glu Thr Gln Glu Leu Glu Ile Ile
                325                 330
```

<210> 15
<211> 1050
<212> DNA
<213> Homo sapiens

<400> 15

```
ccacagcaga gctcacagaa cctgcgggag ccaggctgac ccgccagcat ggtagagttc      60
gcgcccttgt ttgtgccgtg ggagcgcagg ctgcagacac ttgctgtcct acagtttgtc     120
ttctccttct tggcactggg taagatctgc actgtgggct tcatagccct cctgtttaca     180
agattctggc tcctcactgt cctgtatgcg gcctggtggt atctggaccg agacaagcca     240
cggcaggggg gccggcacat ccaggccatc aggtgctgga ctatatggaa gtacatgaag     300
gactatttcc ccatccagct ggtcaagact gctgagctgg acccctctcg gaactacatt     360
gcgggcttcc acccccatgg agtcctggca gtcggagcct ttgccaacct gtgcactgag     420
agcacaggct tctcttcgat cttccccggt atccgccccc atctgatgat gctgaccttg     480
tggttccggg ccccttctt cagagattac atcatgtctg cagggttggt cacatcagaa     540
aaggagagtg ctgctcacat tctgaacagg aagggtggcg gaaacttgct gggcatcatt     600
gtaggggtg cccaggaggc cctggatgcc aggcctggat ccttcacgct gttactgcgg     660
aaccgaaagg gcttcgtcag gctcgccctg acacacgggg caccctggt gccaatcttc     720
tccttcgggg agaatgacct atttgaccag attcccaact cttctggctc ctggttacgc     780
tatatccaga atcggttgca gaagatcatg ggcatctccc tcccactctt tcatggccgt     840
ggtgtcttcc agtacagctt tggtttaata ccctaccgcc ggcccatcac cactgtgggg     900
aagcccatcg aggtacagaa gacgctgcat ccctcggagg aggaggtgaa ccagctgcac     960
cagcattata tcaaagagct gtgcaacctc ttcgaggccc acaaacttaa gttcaacatc    1020
cctgctgacc agcacttgga gttctgctga                                     1050
```

<210> 16
<211> 333
<212> PRT
<213> Homo sapiens

<400> 16

```
Met Val Glu Phe Ala Pro Leu Phe Val Pro Trp Glu Arg Arg Leu Gln
 1               5                  10                  15
Thr Leu Ala Val Leu Gln Phe Val Phe Ser Phe Leu Ala Leu Gly Lys
            20                  25                  30
Ile Cys Thr Val Gly Phe Ile Ala Leu Leu Phe Thr Arg Phe Trp Leu
        35                  40                  45
Leu Thr Val Leu Tyr Ala Ala Trp Trp Tyr Leu Asp Arg Asp Lys Pro
    50                  55                  60
Arg Gln Gly Gly Arg His Ile Gln Ala Ile Arg Cys Trp Thr Ile Trp
65                  70                  75                  80
```

Lys Tyr Met Lys Asp Tyr Phe Pro Ile Gln Leu Val Lys Thr Ala Glu
85 90 95
Leu Asp Pro Ser Arg Asn Tyr Ile Ala Gly Phe His Pro His Gly Val
100 105 110
Leu Ala Val Gly Ala Phe Ala Asn Leu Cys Thr Glu Ser Thr Gly Phe
115 120 125
Ser Ser Ile Phe Pro Gly Ile Arg Pro His Leu Met Met Leu Thr Leu
130 135 140
Trp Phe Arg Ala Pro Phe Phe Arg Asp Tyr Ile Met Ser Ala Gly Leu
145 150 155 160
Val Thr Ser Glu Lys Glu Ser Ala Ala His Ile Leu Asn Arg Lys Gly
165 170 175
Gly Gly Asn Leu Leu Gly Ile Ile Val Gly Gly Ala Gln Glu Ala Leu
180 185 190
Asp Ala Arg Pro Gly Ser Phe Thr Leu Leu Leu Arg Asn Arg Lys Gly
195 200 205
Phe Val Arg Leu Ala Leu Thr His Gly Ala Pro Leu Val Pro Ile Phe
210 215 220
Ser Phe Gly Glu Asn Asp Leu Phe Asp Gln Ile Pro Asn Ser Ser Gly
225 230 235 240
Ser Trp Leu Arg Tyr Ile Gln Asn Arg Leu Gln Lys Ile Met Gly Ile
245 250 255
Ser Leu Pro Leu Phe His Gly Arg Gly Val Phe Gln Tyr Ser Phe Gly
260 265 270
Leu Ile Pro Tyr Arg Arg Pro Ile Thr Thr Val Gly Lys Pro Ile Glu
275 280 285
Val Gln Lys Thr Leu His Pro Ser Glu Glu Glu Val Asn Gln Leu His
290 295 300
Gln His Tyr Ile Lys Glu Leu Cys Asn Leu Phe Glu Ala His Lys Leu
305 310 315 320
Lys Phe Asn Ile Pro Ala Asp Gln His Leu Glu Phe Cys
325 330

<210> 17
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic peptide

<400> 17
Met Gly Asp Tyr Lys Asp Asp Asp Asp Gly
1 5 10

<210> 18
<211> 1233
<212> DNA
<213> Homo sapiens

<400> 18

ttcagccatg aagaccctca tagccgccta ctccggggtc ctgcgcggcg agcgtcaggc 60
cgaggctgac cggagccagc gctctcacgg aggacctgcg ctgtcgcgcg aggggtctgg 120
gagatggggc actggatcca gcatcctctc cgccctccag gacctcttct ctgtcacctg 180
gctcaatagg tccaaggtgg aaaagcagct acaggtcatc tcagtgctcc agtgggtcct 240
gtccttcctt gtactgggag tggcctgcag tgccatcctc atgtacatat tctgcactga 300
ttgctggctc atcgctgtgc tctacttcac ttggctggtg tttgactgga acacacccaa 360
gaaaggtggc aggaggtcac agtgggtccg aaactgggct gtgtggcgct actttcgaga 420
ctactttccc atccagctgg tgaagacaca caacctgctg accaccagga actatatctt 480
tggataccac ccccatggta tcatgggcct gggtgccttc tgcaacttca gcacagaggc 540
cacagaagtg agcaagaagt tcccaggcat acggccttac ctggctacac tggcaggcaa 600
cttccgaatg cctgtgttga gggagtacct gatgtctgga ggtatctgcc ctgtcagccg 660
ggacaccata gactatttgc tttcaaagaa tgggagtggc aatgctatca tcatcgtggt 720
cgggggtgcg gctgagtctc tgagctccat gcctggcaag aatgcagtca ccctgcggaa 780
ccgcaagggc tttgtgaaac tggccctgcg tcatggagct gacctggttc ccatctactc 840
ctttggagag aatgaagtgt acaagcaggt gatcttcgag gagggctcct ggggccgatg 900
ggtccagaag aagttccaga aatacattgg tttcgcccca tgcatcttcc atggtcgagg 960
cctcttctcc tccgacacct gggggctggt gccctactcc aagcccatca ccactgttgt 1020
gggagagccc atcaccatcc ccaagctgga gcacccaacc cagcaagaca tcgacctgta 1080
ccacaccatg tacatggagg ccctggtgaa gctcttcgac aagcacaaga ccaagttcgg 1140
cctcccggag actgaggtcc tggaggtgaa ctgagccagc cttcggggcc aattccctgg 1200
aggaaccagc tgcaaatcac tttttgctc tgt 1233